(handwritten: re-run   see p.5   #4   ENTERED)

```
           RAW SEQUENCE LISTING                DATE: 09/15/2000
           PATENT APPLICATION:   US/09/300,482  TIME: 10:50:56

           Input Set : A:\phosphoglucseq.rpt
           Output Set: N:\CRF3\09152000\I300482.raw
```

```
       2 <110> APPLICANT: Cheikh, Nordine
       3        Liu, Jingdong
       4        Peschke, Virginia M.
       6 <120> TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
       7        Phosphogluconate Pathway
       9 <130> FILE REFERENCE: 04983.0031.US01/38-21(15365)B
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/300,482
C--> 11 <141> CURRENT FILING DATE: 1999-04-28
      11 <160> NUMBER OF SEQ ID NOS: 699
      13 <210> SEQ ID NO: 1
      14 <211> LENGTH: 233
      15 <212> TYPE: DNA
      16 <213> ORGANISM: Zea mays
      18 <400> SEQUENCE: 1
      20 gtttttgcag ttagtagaat atgttagtgg ctcctatgat agggtggaag gatttgagtt   60
      22 attgaatgag gcaatctctg agtatgagac ttcagaaaac aatgactcgg gaagctaccg  120
      24 cagattattt tatttggcat tgcctccatc agtctaccca tcagtatgcg agatgataag  180
      26 atcatattgc atgagtccat cttcacacac cggttggaca agggttattg ttg          233
      29 <210> SEQ ID NO: 2
      30 <211> LENGTH: 180
      31 <212> TYPE: DNA
      32 <213> ORGANISM: Zea mays
      34 <400> SEQUENCE: 2
      36 tcgttcggca gcagcaacga ggtgctggat gggacgccga cgggagatgg ggcaccgggg   60
      38 caggggcagc ggggagcgag caccgtcagc atcacggtcg tcggcgcctc cggcgacctc  120
      40 gccaagaaga agatcttccc ggccctcttc gccttgttct acgagggctg gctcccggag  180
      43 <210> SEQ ID NO: 3
      44 <211> LENGTH: 137
      45 <212> TYPE: DNA
      46 <213> ORGANISM: Zea mays
      48 <400> SEQUENCE: 3
      50 cacagatctt gataggccca ctaatgagct tgtgatacgt gtgcaaccgg atgaagcaat   60
      52 ttacctaaag attaacaaca agattcctgg tctcggtatg cgactagata ggagtaactt  120
      54 gaatctccat tatgccg                                                 137
      57 <210> SEQ ID NO: 4
      58 <211> LENGTH: 263
      59 <212> TYPE: DNA
      60 <213> ORGANISM: Glycine max
      62 <223> OTHER INFORMATION: unsure at all n locations
W--> 63 <400> SEQUENCE: 4
      65 gaagcacttt tggatgttgc gtcatgtctt gcaagcagtg ctcagaccca gaagggatgg   60
      67 aatcgcataa tatttgagaa gccatttggc tttgatgcac tttcttccca taggctgaca  120
W--> 69 caatatcttc tttcaaactt tcaggaaaag caaatatata gaattganca tctactagga  180
W--> 71 aggaatcnca gtnaaaatcc tncaggttta agggtttcaa annnagnttt tgagccacct  240
W--> 73 tngagnngna cntnnnnnga nna                                          263
      76 <210> SEQ ID NO: 5
      77 <211> LENGTH: 259
```

RAW SEQUENCE LISTING   DATE: 09/15/2000
PATENT APPLICATION: US/09/300,482   TIME: 10:50:56

Input Set : A:\phosphoglucseq.rpt
Output Set: N:\CRF3\09152000\I300482.raw

```
        78 <212> TYPE: DNA
        79 <213> ORGANISM: Glycine max
        81 <223> OTHER INFORMATION: unsure at all n locations
W--> 82 <400> SEQUENCE: 5
W--> 84 ctgtgttgag ttttcnancc ttaaaaagac tntctcttct ctctcgtctc tttctctccc   60
W--> 86 tgangcanna nancattagc atgcanancc agagtggttc tagtaatccg gtgctgctag  120
W--> 88 aggntgggaa ctagtgaatg gcatatcgag cgaagatcta gcttcggcac tgaatncccc  180
W--> 90 ttagcaatan aggcangcca tgtgnctgaa actngtcact ctctattgtn gtgcttggcg  240
W--> 92 cttntgggga tcttgctaa                                               259
        95 <210> SEQ ID NO: 6
        96 <211> LENGTH: 284
        97 <212> TYPE: DNA
        98 <213> ORGANISM: Glycine max
       100 <223> OTHER INFORMATION: unsure at all n locations
W--> 101 <400> SEQUENCE: 6
W--> 103 tggaatcgca taatatttga naagccattt ggctttgatg cactttcttc ccataggctg   60
W--> 105 acacaatatc ttctttcaaa ctttcaggaa aagcanatat atagaattga tcanctacta  120
W--> 107 ggaaggaatc ncattgnaaa tcttacagtt tnaaggtttt caaatctagt ttttgagcca  180
W--> 109 ctttggagtc gtacttanat aagataatgt agcaggncat ttatcagagg ncttggctgt  240
W--> 111 gcatcctggg aagntattcn ntggctatgg gatnatccgt ganc                  284
       114 <210> SEQ ID NO: 7
       115 <211> LENGTH: 253
       116 <212> TYPE: DNA
       117 <213> ORGANISM: Glycine max
       119 <223> OTHER INFORMATION: unsure at all n locations
W--> 120 <400> SEQUENCE: 7
W--> 122 gagtgcgtga agaaaacacc aactgttttn agttttccaa ccttaaaaag annnnnnnnn   60
W--> 124 nnnnnnnnnn nnnnnnnnnn nnngaagcaa aanaanatta gcatcaaaac cagagtggtt  120
W--> 126 ctagtaatcc gggngctgcta gaggatggga actagtnaat ggcatatcga gcgaagatct  180
       128 agcttcggca ctgaatcccc cttagcaaga gaggcaggaa atgtgcctga aactgggtca  240
       130 ctctctattg ttg                                                    253
       133 <210> SEQ ID NO: 8
       134 <211> LENGTH: 137
       135 <212> TYPE: DNA
       136 <213> ORGANISM: Glycine max
       138 <400> SEQUENCE: 8
       140 ccaggcagta tataagacat ggacagttga tattctcaga agattttggc actgaaggac   60
       142 gtggcgggta ctttgaccat tatggtatca tgagagacat tatgcagaat catttacttc  120
       144 aaatactagc actcttt                                                137
       147 <210> SEQ ID NO: 9
       148 <211> LENGTH: 287
       149 <212> TYPE: DNA
       150 <213> ORGANISM: Glycine max
       152 <223> OTHER INFORMATION: unsure at all n locations
W--> 153 <400> SEQUENCE: 9
       155 caaccttaaa agactctctt ttctctctct gaactctgaa gcaaaacaac attaccagag   60
       157 tggttctagt aattcagtgc tgctagaaga tggaaactag tgaatggcat atcgagcgaa  120
W--> 159 gatctagctt cggctctgaa tccccttag caaganangc aggaaatgtg cctganactg  180
W--> 161 ggtcactctc tattgtggtg cttggngctt ctggtgatct tgctaagaag aagacatttc  240
```

RAW SEQUENCE LISTING   DATE: 09/15/2000
PATENT APPLICATION: US/09/300,482   TIME: 10:50:56

Input Set : A:\phosphoglucseq.rpt
Output Set: N:\CRF3\09152000\I300482.raw

```
      163 ctgcactttt ccacctatac ctggcaggga ttcttaccac cagatga              287
      166 <210> SEQ ID NO: 10
      167 <211> LENGTH: 251
      168 <212> TYPE: DNA
      169 <213> ORGANISM: Glycine max
      171 <223> OTHER INFORMATION: unsure at all n locations
W--> 172 <400> SEQUENCE: 10
W--> 174 cttttctctc tctgaactct gaagcnaaac aacattacca gagtggttct agtaattcag     60
      176 tgctgctaga agatggaaac tagtgaatgg catatcgagc gaagatctag cttcggctct    120
      178 gaatcccct agcaagagag gcaggaaatg tgcctgaaac tgggtcactc tctattgtgg     180
      180 tgcttggtgc ttctggtgat cttgctaaga agaagacatt tcctgcactt ttccacctat    240
W--> 182 acctgngnta c                                                        251
      185 <210> SEQ ID NO: 11
      186 <211> LENGTH: 193
      187 <212> TYPE: DNA
      188 <213> ORGANISM: Glycine max
      190 <223> OTHER INFORMATION: unsure at all n locations
W--> 191 <400> SEQUENCE: 11
      193 gtttcagcta actctgcttc acttggtaat tgagtggttc tagtaatccg gtgctgctag     60
      195 aggatgggaa ctagtgaatg gcatatcgag cgaagatcta gcttcggcac tgaatcccc    120
W--> 197 ttagcaagat atgcaggaan tgtgcctgaa actgggtcac tctctattgt tgtgcttggc    180
      199 gcttctgggg atc                                                      193
      202 <210> SEQ ID NO: 12
      203 <211> LENGTH: 318
      204 <212> TYPE: DNA
      205 <213> ORGANISM: Zea mays
      207 <223> OTHER INFORMATION: unsure at all n locations
W--> 208 <400> SEQUENCE: 12
W--> 210 gcgagccaag agcgtggaga ntngatggaa ccttaacctc gcagagcttg ccaggatntg     60
      212 gaaggcggc tgcattatcc gtgcgaggtt ccttgatagg atcaagagcg cgtacgacag    120
      214 gaatcctgag ctcgccaatg gcgcagccat ttgaggaatt ggttggtatg agcagggatg    180
      216 ttttctgctt tgggtgattt ctctctgtgg gttatctttc cttttactat tgttatcttt    240
      218 atgcttctag atccaagtcg agtacttcga ataatgctgt actgtatggt tggcaagtga    300
      220 agaacattgt gtagcttc                                                  318
      223 <210> SEQ ID NO: 13
      224 <211> LENGTH: 467
      225 <212> TYPE: DNA
      226 <213> ORGANISM: Zea mays
      228 <223> OTHER INFORMATION: unsure at all n locations
W--> 229 <400> SEQUENCE: 13
      231 ggccaagagc gcggagaaag gctgggggct caacccgctc gtccttcagc ccgctcagga     60
      233 acctcgagtc caaggacgcc tcgatcgtag gagcggccac cgacagctcg gcggcctgct    120
      235 gcaccgtcca cttccctgtc cctttcatcc cggtcttgtc aaggaccttg tccaccaggt    180
W--> 237 agccatcgcc atgctcgtcc ttgatgccaa agatgtcggc cgtgatctcn atcaagaagc    240
      239 tcaggagctc gcccttgttc cactcggaga cacctggtg cagctcactg ttggtgagct    300
W--> 241 taccgaccga cttgagaacg tcgtatgcct nggaaatcaa ctgcatatcg gcatactcga    360
W--> 243 ttccgttggt gaaccatttt nacaaaantt ncccgatnca nctttngcca agtacgtnaa    420
W--> 245 acaaangggc cacttttaa ggggccttta anaaancncc tttnnng                   467
      248 <210> SEQ ID NO: 14
```

RAW SEQUENCE LISTING   DATE: 09/15/2000
PATENT APPLICATION: US/09/300,482   TIME: 10:50:56

Input Set : **A:\phosphoglucseq.rpt**
Output Set: **N:\CRF3\09152000\I300482.raw**

```
      249 <211> LENGTH: 410
      250 <212> TYPE: DNA
      251 <213> ORGANISM: Zea mays
      253 <223> OTHER INFORMATION: unsure at all n locations
W--> 254 <400> SEQUENCE: 14
      256 cccacgcgtc cgcggtcatg gggcagaacc ttgccctcaa cattgcagag aaagggttcc    60
      258 ccatctctgt gtacaacagg acaacctcca aggtggacga gaccgtgcag cgtgccaagg   120
      260 cagaaggaaa ccttcccgtc tacggcttcc atgaccccgc gtcctttgtg aagtccattc   180
      262 agaagccacg ggtggtgatc atgctcgtca aggccggcgc gccagttgac cagaccatcg   240
      264 cgacgctcgc agctcacttg gagcagggcg actgcatcat cgatggggg aacgagtggt   300
W--> 266 acgagaacac ggagaggagg gagaaggcca tggaggagcg cggcctnctg tatcttggca   360
      268 tgggtgtctc tggaggaaag gagggtgccc gcaacggccc gtccttgatg              410
      271 <210> SEQ ID NO: 15
      272 <211> LENGTH: 449
      273 <212> TYPE: DNA
      274 <213> ORGANISM: Zea mays
      276 <400> SEQUENCE: 15
      278 cccacgcgtc cgcccacgcg ttcgggtggt ttgacggtgc tggcatcgcc aattcaactc    60
      280 cgcatctgca tcggcagcgc gccagctcca tagtgtagga ggagatggcg ctcacaagaa   120
      282 tcggtcttgc tggccttgcg gtcatggggc agaaccttgc cctcaacatt gcagagaaag   180
      284 ggttccccat ctctgtgtac aacaggacaa ccttcaaggt ggacgagacc gtgcagcgtg   240
      286 ccaaggcaga aggaaacctt cccgtctacg gcttccatga ccccgcgtcc tttgtgaagt   300
      288 ccattcagaa gccacgggtg gtgatcatgc tcgtcaaggc cggcgcgcca gttgaccaga   360
      290 ccatcgcgac gctcgcagct cacttggagc agggcgactg catcatcgat aggggggaacg   420
      292 agtggtacga gaacacggag aggagggag                                      449
      295 <210> SEQ ID NO: 16
      296 <211> LENGTH: 410
      297 <212> TYPE: DNA
      298 <213> ORGANISM: Zea mays
      300 <400> SEQUENCE: 16
      302 ggcactttcc ctgcctgatt ggcgatttaa gcggtggggg agggaaggcc gatggtcagt    60
      304 gaaagagagt aggtggacgg acggtgctgg catcgccaat tcaactccgc atctgcatcg   120
      306 gcagcgcgcc agctccatag tgtaggagga gatggcgctc acaagaatcg gtcttgctgg   180
      308 ccttgcggtc atggggcaga accttgccct caacattgca gagaaagggt tccccatctc'   240
      310 tgtgtacaac aggacaacct ccaaggtgga cgagaccgtg cagcgtgcca aggcagaagg   300
      312 aaaccttccc gtctacggct tccatgaccc cgcgtccttt gtgaagtcca ttcagaagcc   360
      314 acgggtggtg atcatgctcg tcaaggccgg cgcgccagtt gaccagacca              410
      317 <210> SEQ ID NO: 17
      318 <211> LENGTH: 409
      319 <212> TYPE: DNA
      320 <213> ORGANISM: Zea mays
      322 <400> SEQUENCE: 17
      324 aggtggccgg acggtggtgg catcgccaat tcaactccgc atctgaatcg gcactcggca    60
      326 gcgcgccagc tccatagtgt aggaggagga gatggcgctc acaagaatcg gtcttgctgg   120
      328 ccttgcggtc atggggcaga accttgccct caacattgca gagaaagggt tccccatctc   180
      330 tgtgtacaac aggacaacct ccaaggtgga cgagaccgtg cagcgtgcca aggcagaagg   240
      332 aaaccttccc gtctacggct tccatgaccc cgcgtccttt gtgaactcca ttcagaagcc   300
      334 acgggtggtg atcatgctcg tcaaggccgg cgcgccagtt gaccagacca tcgcgacgct   360
      336 cgcagctcac ttggagcagg gcgactgcat catcgaatgg gggaacgag                409
```

```
        RAW SEQUENCE LISTING              DATE: 09/15/2000
        PATENT APPLICATION:   US/09/300,482   TIME: 10:50:56

        Input Set : A:\phosphoglucseq.rpt
        Output Set: N:\CRF3\09152000\I300482.raw
```

```
339 <210> SEQ ID NO: 18
340 <211> LENGTH: 420
341 <212> TYPE: DNA
342 <213> ORGANISM: Zea mays
344 <400> SEQUENCE: 18
346 ggtggacgga cggtgctggc atcgccaatt caacttcgca tctgcatcgg cagcgcgcca    60
348 gctccatagg aggagatggc gctcacaaga atcggtcttg ctggccttgc ggtcatgggg   120
350 cagaaccttg ccctcaacat tgcagagaaa gggttcccca tctctgtgta caacaggaca   180
352 acctccaagg tggacgagac cgtgcagcgt gccaaggcag aaggaaacct tcccgtctac   240
354 ggcttccatg accccgcgtc ctttgtgaag tccattcaga agccacgggt ggtgatcatg   300
356 ctcgtcaagg ccggcgcgcc agttgaccag accatcgcga cgctcgcagc tcacttggag   360
358 cagggcgact gcatcatcga taggggaac gagtggtacg aggacacgga gaggagggag   420
361 <210> SEQ ID NO: 19
362 <211> LENGTH: 403
363 <212> TYPE: DNA
364 <213> ORGANISM: Zea mays
366 <400> SEQUENCE: 19
368 agcggacgcg tgggggacgg acggtgctgg catcgccaat tcaactccgc atctgcatcg    60
370 gcagcgcgcc agctccatag tgtaggagga gatgcgctc acaagaatcg gtcttgctgg   120
372 ccttgcggtc atggggcaga accttgccct caacattgca gagaaagggt tccccatctc   180
374 tgtgtacaac aggacaacct ccaaggtgga cgagaccgtg cagcgtgcca aggcagaagg   240
376 aaaccttccc gtctacggct tccatgaccc cgcgtccttt gtgaagtcca ttcagaagcc   300
378 acgggtggtg atcatgctcg tcaaggccgg cgcgccagtt gaccagacca tcgcgacgct   360
380 cgcagctcac tttgagcagg gcgactgcat catcgatggg ggg                    403
383 <210> SEQ ID NO: 20
384 <211> LENGTH: 433
385 <212> TYPE: DNA
386 <213> ORGANISM: Zea mays
388 <400> SEQUENCE: 20
390 ggcactttcc ctgcctgatt ggcgatttat agcggtgggg gagggaaggc cgatggtcag    60
392 ggaaagagag taggtggacg gacggtgctg gcatcgccaa ttcaactccg catctgcatc   120
394 ggcagcgcgc cagctccata ggaggagatg gcgctcacaa gaatcggtct tgctggcctt   180
396 gcggtcatgg ggcagaacct tgccctcaac attgcagaga aagggttccc catctctgtg   240
398 tacaacagga caacctccaa ggtggacgag accgtgcagc gtgccaaggc agaaggaaac   300
400 cttcccgtct acggcttcca tgaccccgcg tcctttgtga agtccattca gaagccacgg   360
402 gtggtgatca tgctcgtcaa ggccggcgcg ccagttgacc agaccatcgc gacgctcgca   420
404 gctcacttgg agc                                                     433
407 <210> SEQ ID NO: 21
408 <211> LENGTH: 209
409 <212> TYPE: DNA
410 <213> ORGANISM: Zea mays
412 <223> OTHER INFORMATION: unsure at all n locations
W--> 413 <400> SEQUENCE: 21
W--> 415 gcatctgcat cggcagcgcg ncagnngnat aggaggagat ggcgctcaca agaatcggtn    60
W--> 417 ttgctggcct tgcggncatg gggcagaacc ttgccctnaa cattgcagag aaagggnnan   120
W--> 419 ccatatgtgt gnacaacagg acaacctgca aggtngacna gaccgtncag ngngncnagg   180
W--> 421 cagaangana ccttangntt tannnattg                                    209
424 <210> SEQ ID NO: 22
425 <211> LENGTH: 271
```

FYI

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

```
                    VERIFICATION SUMMARY              DATE: 09/15/2000
                    PATENT APPLICATION:   US/09/300,482      TIME: 10:50:57

                    Input Set : A:\phosphoglucseq.rpt
                    Output Set: N:\CRF3\09152000\I300482.raw
```

```
L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:63 M:283 W: Missing Blank Line separator, <400> field identifier
L:69 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:69 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:69 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:69 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
L:71 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:71 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:71 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
M:340 Repeated in SeqNo=4
L:73 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:73 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:73 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:82 M:283 W: Missing Blank Line separator, <400> field identifier
L:84 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:84 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:84 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:84 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
L:86 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:86 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:86 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
M:340 Repeated in SeqNo=5
L:88 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:88 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:88 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:90 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:90 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:90 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:92 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:92 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:92 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:101 M:283 W: Missing Blank Line separator, <400> field identifier
L:103 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:103 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:103 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:103 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:105 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:105 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:105 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
M:340 Repeated in SeqNo=6
L:107 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:107 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:107 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:109 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:109 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:109 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:111 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
```

VERIFICATION SUMMARY   DATE: 09/15/2000
PATENT APPLICATION: US/09/300,482 TIME: 10:50:57

Input Set : A:\phosphoglucseq.rpt
Output Set: N:\CRF3\09152000\I300482.raw

```
L:111 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:111 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:120 M:283 W: Missing Blank Line separator, <400> field identifier
L:122 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7
L:122 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:122 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:122 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7
L:124 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7
L:124 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:124 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
M:340 Repeated in SeqNo=7
L:126 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7
L:126 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:126 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:153 M:283 W: Missing Blank Line separator, <400> field identifier
L:159 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:9
L:159 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
L:159 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
M:340 Repeated in SeqNo=9
L:172 M:283 W: Missing Blank Line separator, <400> field identifier
L:174 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10
M:340 Repeated in SeqNo=10
L:191 M:283 W: Missing Blank Line separator, <400> field identifier
L:197 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
L:208 M:283 W: Missing Blank Line separator, <400> field identifier
L:210 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:12
L:229 M:283 W: Missing Blank Line separator, <400> field identifier
L:237 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13
M:340 Repeated in SeqNo=13
L:254 M:283 W: Missing Blank Line separator, <400> field identifier
L:266 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:14
L:413 M:283 W: Missing Blank Line separator, <400> field identifier
L:415 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:21
M:340 Repeated in SeqNo=21
L:430 M:283 W: Missing Blank Line separator, <400> field identifier
L:432 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:22
M:340 Repeated in SeqNo=22
L:465 M:283 W: Missing Blank Line separator, <400> field identifier
L:471 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:24
M:340 Repeated in SeqNo=24
L:600 M:283 W: Missing Blank Line separator, <400> field identifier
L:608 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:32
M:340 Repeated in SeqNo=32
L:685 M:283 W: Missing Blank Line separator, <400> field identifier
L:691 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:37
L:756 M:283 W: Missing Blank Line separator, <400> field identifier
L:758 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:41
M:340 Repeated in SeqNo=41
L:1105 M:283 W: Missing Blank Line separator, <400> field identifier
```

VERIFICATION SUMMARY   DATE: 09/15/2000
PATENT APPLICATION: US/09/300,482   TIME: 10:50:57

Input Set : A:\phosphoglucseq.rpt
Output Set: N:\CRF3\09152000\I300482.raw

L:1113 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:61
L:1142 M:283 W: Missing Blank Line separator, <400> field identifier
L:1148 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:63
M:340 Repeated in SeqNo=63
L:1197 M:283 W: Missing Blank Line separator, <400> field identifier
L:1199 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:66
M:340 Repeated in SeqNo=66
L:1320 M:283 W: Missing Blank Line separator, <400> field identifier
L:1322 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:73
M:340 Repeated in SeqNo=73
L:1375 M:283 W: Missing Blank Line separator, <400> field identifier
L:1377 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:76
M:340 Repeated in SeqNo=76
L:1820 M:283 W: Missing Blank Line separator, <400> field identifier
L:1824 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:101
L:1861 M:283 W: Missing Blank Line separator, <400> field identifier
L:1875 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:103
L:1916 M:283 W: Missing Blank Line separator, <400> field identifier
L:1918 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:106
M:340 Repeated in SeqNo=106
L:1935 M:283 W: Missing Blank Line separator, <400> field identifier
L:1939 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:107
M:340 Repeated in SeqNo=107
L:2458 M:283 W: Missing Blank Line separator, <400> field identifier
L:2464 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:138
M:340 Repeated in SeqNo=138
L:2479 M:283 W: Missing Blank Line separator, <400> field identifier
L:2489 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:139
M:340 Repeated in SeqNo=139
L:2500 M:283 W: Missing Blank Line separator, <400> field identifier
L:2506 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:140
L:2611 M:283 W: Missing Blank Line separator, <400> field identifier
L:2613 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:146
M:340 Repeated in SeqNo=146
L:2870 M:283 W: Missing Blank Line separator, <400> field identifier
L:2891 M:283 W: Missing Blank Line separator, <400> field identifier
L:2912 M:283 W: Missing Blank Line separator, <400> field identifier
L:3097 M:283 W: Missing Blank Line separator, <400> field identifier
L:3134 M:283 W: Missing Blank Line separator, <400> field identifier
L:3721 M:283 W: Missing Blank Line separator, <400> field identifier
L:3806 M:283 W: Missing Blank Line separator, <400> field identifier
L:4131 M:283 W: Missing Blank Line separator, <400> field identifier
L:4300 M:283 W: Missing Blank Line separator, <400> field identifier
L:4357 M:283 W: Missing Blank Line separator, <400> field identifier
L:4446 M:283 W: Missing Blank Line separator, <400> field identifier
L:4631 M:283 W: Missing Blank Line separator, <400> field identifier
L:4676 M:283 W: Missing Blank Line separator, <400> field identifier
L:4739 M:283 W: Missing Blank Line separator, <400> field identifier
L:4758 M:283 W: Missing Blank Line separator, <400> field identifier

VERIFICATION SUMMARY   DATE: 09/15/2000
PATENT APPLICATION: US/09/300,482 TIME: 10:50:57

Input Set : A:\phosphoglucseq.rpt
Output Set: N:\CRF3\09152000\I300482.raw

L:4795 M:283 W: Missing Blank Line separator, <400> field identifier
L:4900 M:283 W: Missing Blank Line separator, <400> field identifier
L:4919 M:283 W: Missing Blank Line separator, <400> field identifier
L:4956 M:283 W: Missing Blank Line separator, <400> field identifier
L:4975 M:283 W: Missing Blank Line separator, <400> field identifier
L:5210 M:283 W: Missing Blank Line separator, <400> field identifier